

## Sequence analysis

Advance Access publication October 6, 2014

# Chimera: a Bioconductor package for secondary analysis of fusion products

Marco Beccuti<sup>1</sup>, Matteo Carrara<sup>2</sup>, Francesca Cordero<sup>1</sup>, Fulvio Lazzarato<sup>3,4</sup>,  
Susanna Donatelli<sup>1</sup>, Francesca Nadalin<sup>5</sup>, Alberto Policriti<sup>6</sup> and Raffaele A. Calogero<sup>2,\*</sup><sup>1</sup>Department of Computer Sciences, University of Torino, C.so Svizzera 185, 10149 Torino, <sup>2</sup>Department of Molecular Biotechnology and Health Sciences, University of Torino, Via Nizza 52, 10126 Torino, <sup>3</sup>Department of Translational Medicine, University of Piemonte Orientale Avogadro, Novara, <sup>4</sup>Unit of Cancer Epidemiology, Department of Medical Sciences, University of Turin, Turin, <sup>5</sup>Department of Computational and Quantitative Biology, UMR 7238 CNRS - Université Pierre et Marie Curie, Paris, France and <sup>6</sup>Department of Mathematics and Computer Science, University of Udine, Italy

Associate Editor: Gunnar Ratsch

**ABSTRACT**

**Summary:** *Chimera* is a Bioconductor package that organizes, annotates, analyses and validates fusions reported by different fusion detection tools; current implementation can deal with output from bellerophon, chimeraScan, deFuse, fusionCatcher, FusionFinder, FusionHunter, FusionMap, mapSplice, Rsubread, tophat-fusion and STAR. The core of *Chimera* is a fusion data structure that can store fusion events detected with any of the aforementioned tools. Fusions are then easily manipulated with standard R functions or through the set of functionalities specifically developed in *Chimera* with the aim of supporting the user in managing fusions and discriminating false-positive results.

**Availability and implementation:** *Chimera* is implemented as a Bioconductor package in R. The package and the vignette can be downloaded at [bioconductor.org](http://bioconductor.org).

**Contact:** [raffaele.calogero@unito.it](mailto:raffaele.calogero@unito.it)

**Supplementary information:** Supplementary data are available at *Bioinformatics* online.

Received on March 19, 2014; revised on September 30, 2014; accepted on October 1, 2014

## 1 INTRODUCTION

Fusion genes, also known as chimeras, have become crucial in the areas of biomarkers and therapeutic targets investigation. The emergence of deep sequencing of the transcriptome has opened many opportunities for the identification of this class of genomic alterations, leading to the discovery of novel chimeric transcripts in cancers. A significant number of bioinformatics algorithms have been developed to detect fusion genes (Beccuti *et al.*, 2013). Recently, we have shown that the performances of such tools can be quite variegated and that their false-positive detection rate can be a critical issue (Carrara *et al.*, 2013) (Carrara *et al.*, 2013). Most tools detect fusion events in two steps: (i) alignment to a reference genome to detect discordant alignments, and (ii) refinements of fusion candidates with removal of false-positive results. The second step is particularly critical, as each tool implements a different set of filters (Beccuti

*et al.*, 2013; Wang *et al.*, 2013), and users have limited control on them. As each fusion detection tool has a specific combination of alignment and filtering approaches, results produced by each tool are only partially comparable with the others' (Carrara *et al.*, 2013a,b). Thus, although the combination of the results derived from different tools can increase the number of true fusions detected, it also significantly increases the number of false-positive results (see Supplementary Material). The Bioconductor package *Chimera*, reported in this note, provides a common framework to manipulate, analyze and filter fusion events detected by a variety of fusion detection tools. *Chimera* is based on typical R data structures, which allows its users to take advantage also of the full set of R functionalities.

## 2 DESCRIPTION

The flow of analysis supported by *Chimera* is described in Figure 1, and it is exemplified in the note's Supplementary Material. With the functions made available by *Chimera*, the user can import data from 11 different fusion detection tools, represented on top of Figure 1, into a list of fusions. Each fusion stores the genomic break point and all the information that can be derived from the output of fusion detection tools (e.g. number of spanning and encompassing reads supporting the fusion junction, splicing pattern used and transcripts involved in the fusion). As each fusion detection tool might rely on different gene annotations, the import function recovers the HUGO (Seal *et al.*, 2011) symbols for the genes involved in the fusion, by overlapping the fusion break points to the genes' genomic location stored in the Bioconductor package (Gentleman *et al.*, 2004) [org.Hs.eg.db](http://org.Hs.eg.db), which contains a genome-wide annotation based on Entrez Gene identifiers.

Thus, a fusion involving two annotated genes will be described as SymbolX:SymbolY. In case a break point is located in a non-coding genomic region, it is annotated using its genomic coordinates (e.g. NBPF1:chr14:81937890-81937920).

A list of fusions can be manipulated, as in Figure 1, using basic R list functions (e.g. concatenation) or with the set of *Chimera* 'fusion queries', e.g. function *fusionName* extracts the fusion name in the above described format (e.g. SPDYE8P:SLC24A5), function *prettyPrint* stores fusions

\*To whom correspondence should be addressed.

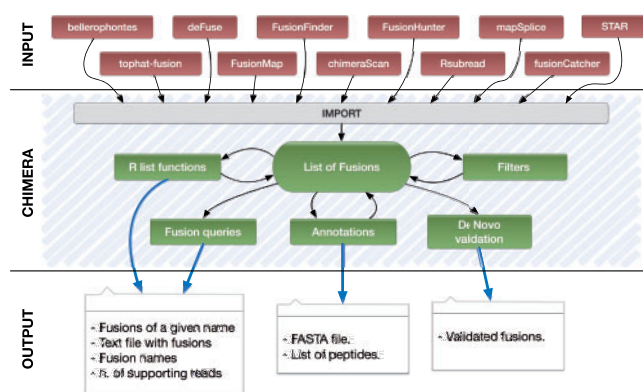


Fig. 1. The information flow in *Chimera*

description in a tab delimited file and function *supportingReads* extracts supporting reads for a given fusion.

## 2.1 Fusion filtering

Once the user has created and inspected the fusion list with the above functionalities, he/she might decide to filter the fusions through a select/exclude mechanism. Available filtering criteria are as follows: (i) a (user defined) threshold for the number of encompassing/spanning reads; (ii) a specific subset of fusion names; (iii) the presence of annotated gene names in fusions (e.g. SPDY8P:SLC24A5 is kept, NBPFL:chr14:81937890-81937920 is excluded); (iv) fusions belonging to long distance exons of the same gene (e.g. SPDY8P:SPDY8P is discarded) and (v) presence of an intron at the fusion junction. This last filter is justified by the fact that analysis is performed on mature mRNAs. Thus, in case long introns are retained at the fusion break point, it is likely that such fusion event will not be translated into a functional protein.

## 2.2 Annotation

A user willing to complete, or enrich, fusion data can use *Chimera* functionalities for annotation ('Annotations' block in Fig. 1). The annotation facility allows to generate (i) the nucleotide sequence of a (list of) fusions (*chimeraSeqSet*); (ii) the number of supporting reads; and (iii) the list of fusion encoded peptides.

This additional information could be used as final output or to enrich the information present in a fusion object. In particular, the output of *chimeraSeqSet* is a R DNASTringSet object that can be exported as a fasta file and that can enrich the fusion information (with the method *addRNA*). This output can also be used by the function *fusionPeptides* to explore the fusion at the protein level (the function retrieves the peptide regions involved and evaluates whether the fusion will produce an in-frame polypeptide). *Chimera* also embeds *Oncofuse* (Shugay *et al.*, 2013), a naive Bayes Network Classifier that provides a variegated annotation of fusions, as well as a score for the probability that a fusion acts as tumor driver.

## 2.3 Validation

Finally, a user can take advantage of *Chimera* to perform a first step of validation, which can be useful given the high number of false-positive results reported, in most cases, by fusion detection tools. Fusion break points are assessed by *de novo* assembly using GapFiller (Nadalin *et al.*, 2012). GapFiller is a seed-and-extend method able to correctly fill the gap between paired reads, thus it generates accurate longer sequences with respect to input reads.

The supporting reads of a fusion (whether made available by the fusion detection tool or through the *Chimera* annotation functions) are assembled with GapFiller into a reference. The nucleotide sequence of the fusion break point, reconstructed by *chimeraSeqSet*, is then checked for inclusion against the *de novo* assembled reference. Validation is particularly useful for the correct evaluation of fusion events supported by few reads (see Supplementary Material).

## 3 DISCUSSION

To the best of our knowledge, *Chimera* is the only available software able to integrate and compare the data produced by different fusion detection tools. Thus, it represents an answer to the lack of standard data structure for fusion data representation. Furthermore, as the combination of results from more than one fusion detection tool enhances the probability to identify fusion events (see Supplementary Material), *Chimera* provides a common framework to manipulate, filter and prioritize fusion events. Moreover *Chimera* offers a validation procedure based on *de novo* assembly (thanks to the GapFiller tool) and enhances fusions' annotation through the exploitation of the Oncofuse results.

**Funding:** This work was supported by the Epigenomics Flagship Project EPIGEN and the European 7th frame-work program, Health.2012.1.2-1, NGS-PTL grant n. 306242.

**Conflict of interest:** none declared.

## REFERENCES

- Beccuti, M. *et al.* (2013) The structure of state-of-art gene fusion-finder algorithms. *Genome Bioinformatics*, **1**, 2.
- Carrara, M. *et al.* (2013a) State of art fusion-finder algorithms are suitable to detect transcription-induced chimeras in normal tissues? *BMC Bioinformatics*, **14** (Suppl. 7), S2.
- Carrara, M. *et al.* (2013b) State-of-the-art fusion-finder algorithms sensitivity and specificity. *Biomed. Res. Int.*, **2013**, 340620.
- Gentleman, R.C. *et al.* (2004) Bioconductor: open software development for computational biology and bioinformatics. *Genome Biol.*, **5**, R80.
- Nadalin, F. *et al.* (2012) GapFiller: a de novo assembly approach to fill the gap within paired reads. *BMC Bioinformatics*, **13** (Suppl. 14), S8.
- Seal, R.L. *et al.* (2011) genenames.org: the HGNC resources in 2011. *Nucleic Acids Res.*, **39**, D514–D519.
- Shugay, M. *et al.* (2013) Oncofuse: a computational framework for the prediction of the oncogenic potential of gene fusions. *Bioinformatics*, **29**, 2539–2546.
- Wang, Q. *et al.* (2013) Application of next generation sequencing to human gene fusion detection: computational tools, features and perspectives. *Brief. Bioinform.*, **14**, 506–519.